

APRIL/MAY 2023

**CBT53 — BIOINFORMATICS**

Time : Three hours

Maximum : 75 marks

SECTION A — (10 × 2 = 20 marks)

Answer ALL questions.

1. What are the uses of NCBI?
2. Summarize about specialized databases.
3. Recall the formula of Needleman wunsch algorithm.
4. Compare Global and local alignment with examples.
5. Name any three gene prediction methods.
6. Outline the significance of comparative genomics.
7. List out the features of Rasmol.
8. Compare SCOP and CATH.
9. Define comparative modeling.
10. Summarize about alpha helix.



**SECTION B — (5 × 5 = 25 marks)**

Answer ALL questions.

11. (a) Organize the applications of Bio informatics in various fields.

Or

(b) List out the protein primary databases and explain.

12. (a) Utilize progressive alignment for phylogenetic tree construction.

Or

(b) Construct the steps in dot plot method to compare two sequences with an example.

13. (a) Categorize the steps in performing FASTA.

Or

(b) List out any three genomic analysis tools and explain any one.

14. (a) Identify the features of protein structure database.

Or

(b) Categorize the applications of protein visualization tools.

15. (a) How will you utilize the tools to predict protein functions.

Or

(b) Compare Steps in ab initio modelling and fold recognition method.

**SECTION C — (3 × 10 = 30 marks)**

Answer any THREE questions.

16. Explain in detail about Biological databases.

17. Compare pair wise and multiple sequence alignment.

18. Explain the steps of BLAST algorithm and its applications.

19. Elaborate in detail protein classification based on structure.

20. Discuss in detail about steps in homology modeling.

